CD105PCT.ST25.txt

SEQUENCE LISTING

<110> CropDesign N.V.

<120> Plants having modified growth characteristics and method for making the same

<130> CD-105-PCT

<150> US 60/528,113
<151> 2003-12-09

<150> EP 03104280.7
<151> 2003-11-19

<160> 18

<170> PatentIn version 3.3

<210> 1
<211> 1428
<212> DNA
<213> Nicotiana tabacum

<220>
<221> misc_feature
<223> seedyl coding sequence (CDS0689)

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ccacttaacc ctaatggggc tctggaaaat tcaagactca agccgaacaa gcccaattcc 300
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gagaagaaaa tagacgagga aattgaagaa attcagatgg agattagtag gttgagttca 420
agattagagg ctttgagaat tgaaaaggct gagaaaactg ttgctaagac tgttgaaaag 480
cgaggaaggg ttgtggcagc aaagtttatg gagccaaaac aaagtgttat taagattgaa 540
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ccatctgaga tttttactgg aacgcggcgg cgagggttga gtatggggcc atcagatatt 660
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aagaagcccc agaggccggg gagggttgtg gctagtaggt ataatcagag tacaattcag 1020
tcatcagtag tgagaaagag gtctttacct gaaaatgata aggatgagag taagagaaat 1080
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<210> 2
<211> 475
<212> PRT
<213> Nicotiana tabacum

<220>
<221> MISC_FEATURE
<223> seedyl protein (CDS0689)

<400> 2

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Ile Trp Asn Asn Ala Ala Phe Asp Asn Gly Asp Ser Glu Asp Leu Ser
            20                  25                  30

Ser Leu Lys Arg Ser Trp Ser Pro Leu Lys Pro Leu Ser Val Arg Pro
        35                  40                  45

Ser Asp Ser Phe Glu Ser Asp Leu Ser Ser Lys Glu Asn Gln Thr Pro
    50                  55                  60

Leu Phe Glu Asn Ser Ser Val Asn Leu Ser Ser Pro Leu Pro Ile Lys
65                  70                  75                  80

Pro Leu Asn Pro Asn Gly Ala Leu Glu Asn Ser Arg Leu Lys Pro Asn
                85                  90                  95

Lys Pro Asn Ser Lys Gln Ser Leu Asp Glu Met Ala Ala Arg Lys Ser
            100                 105                 110

Gly Lys Gly Asn Asp Phe Arg Asp Glu Lys Lys Ile Asp Glu Glu Ile
        115                 120                 125

Glu Glu Ile Gln Met Glu Ile Ser Arg Leu Ser Ser Arg Leu Glu Ala
    130                 135                 140

Leu Arg Ile Glu Lys Ala Glu Lys Thr Val Ala Lys Thr Val Glu Lys
145                 150                 155                 160

Arg Gly Arg Val Val Ala Ala Lys Phe Met Glu Pro Lys Gln Ser Val
                165                 170                 175

Ile Lys Ile Glu Glu Arg Ile Ser Met Ser Ala Arg Thr Lys Val Glu
            180                 185                 190

Gln Arg Arg Gly Leu Ser Leu Gly Pro Ser Glu Ile Phe Thr Gly Thr
        195                 200                 205

Arg Arg Arg Gly Leu Ser Met Gly Pro Ser Asp Ile Leu Ala Gly Thr
    210                 215                 220

Thr Lys Ala Arg Gln Leu Gly Lys Gln Glu Met Ile Ile Thr Pro Ile
225                 230                 235                 240

Gln Pro Ile Gln Asn Arg Arg Lys Ser Cys Phe Trp Lys Leu Gln Glu
                245                 250                 255

Ile Glu Glu Glu Gly Lys Ser Ser Ser Leu Ser Pro Lys Ser Arg Lys
            260                 265                 270

Thr Ala Ala Arg Thr Met Val Thr Thr Arg Gln Ala Val Thr Thr Ile
        275                 280                 285
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Ala Ser Lys Lys Asn Leu Lys Lys Asp Asp Gly Leu Leu Ser Ser Val
    290                 295                 300

Gln Pro Lys Lys Leu Phe Lys Asp Leu Glu Lys Ser Ala Ala Ala Asn
305                 310                 315                 320

Lys Lys Pro Gln Arg Pro Gly Arg Val Val Ala Ser Arg Tyr Asn Gln
                325                 330                 335

Ser Thr Ile Gln Ser Ser Val Val Arg Lys Arg Ser Leu Pro Glu Asn
            340                 345                 350

Asp Lys Asp Glu Ser Lys Arg Asn Asp Lys Lys Arg Ser Leu Ser Val
        355                 360                 365

Gly Lys Thr Arg Val Ser Gln Thr Glu Ser Lys Asn Leu Gly Thr Glu
    370                 375                 380

Ser Arg Val Lys Lys Arg Trp Glu Ile Pro Ser Glu Ile Val Val His
385                 390                 395                 400

Gly Asn Thr Glu Ser Glu Lys Ser Pro Leu Ser Ile Ile Val Lys Pro
                405                 410                 415

Asp Leu Leu Pro Arg Ile Arg Ile Ala Arg Cys Val Asn Glu Thr Leu
            420                 425                 430

Arg Asp Ser Gly Pro Ala Lys Arg Met Ile Glu Leu Ile Gly Lys Lys
        435                 440                 445

Ser Phe Phe Ser Ser Asp Glu Asp Lys Glu Pro Pro Val Cys Gln Val
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Leu Ser Phe Ala Glu Glu Asp Ala Glu Glu Glu
465                 470                 475
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<210> 3
<211> 1336
<212> DNA
<213> Oryza sativa

<220>
<221> misc_feature
<223> seedyl coding sequence

<400> 3

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ggcgacaagg agaatcaccg ccccgaggtt gttgatgtcg ccgccggcta cgacgtcgag    180
gccgagatcg gccacatcga ggcggagatc ctgcgcctct cgtcccggct ccaccatctc    240
cgcgtctcca agcagccgga gcccaaccgc gacgacgctc cgatgggggga gatggtcgcg    300
aaggtgaggc cccggccgag gggcctcagc ctcgggcccc tggatgtgat ctccatcgtc    360
aatcgtgaga agcatccgct gcgcaccaag cagcctccgg cgacgcgggg caggggctc     420
agcctcgggc ccatggagat cgccgcggcg aaccctaggg tgcccgcggc ggcgcagcat    480
cagcaacagc aacgcgctgg cacggcgcgg atcctgaagc caatcaagga gcctccggtg    540
cagcgtcgca ggggcgtcag cctcgggccg ttggagatcc accacggcgt cggcagcaag    600
gcaccagcgg cggcgcgagc caagccgttc accaccaagc tcaacgccat tcgagaagaa    660
acccgaccct ccaagcaatt cgccgtcccc gccaagccat ggccgtcgag caatacaagg    720
cagacactgg actcgaggca aggaacagca gcaagtcgag cgaaggcgag gagcccgagc    780
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gccactgcca agaggatggc ggggagctcc aagatgaggg tcatcccgag ccgctacagc 960
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gccgaattgg tcgggaagcg ctcgttcttc acggctgcag ccgaggacgg gcgggcgctc 1260
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ttccttccat cagctc 1336

<210> 4
<211> 431
<212> PRT
<213> Oryza sativa

<220>
<221> MISC_FEATURE
<223> seedyl protein

<400> 4

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Ala Phe Asp Asp Ser Ser Cys Ser Arg Ser Ala Trp Leu Pro Gln Ser
20 25 30

Pro Ala Val Ala Ala Val Arg Lys Gly Asp Lys Glu Asn His Arg Pro
35 40 45

Glu Val Val Asp Val Ala Ala Gly Tyr Asp Val Glu Ala Glu Ile Gly
50 55 60

His Ile Glu Ala Glu Ile Leu Arg Leu Ser Ser Arg Leu His His Leu
65 70 75 80

Arg Val Ser Lys Gln Pro Glu Pro Asn Arg Asp Asp Ala Pro Met Gly
85 90 95

Glu Met Val Ala Lys Val Arg Pro Arg Pro Arg Gly Leu Ser Leu Gly
100 105 110

Pro Leu Asp Val Ile Ser Ile Val Asn Arg Glu Lys His Pro Leu Arg
115 120 125

Thr Lys Gln Pro Pro Ala Thr Arg Gly Arg Gly Leu Ser Leu Gly Pro
130 135 140

Met Glu Ile Ala Ala Ala Asn Pro Arg Val Pro Ala Ala Ala Gln His
145 150 155 160

Gln Gln Gln Gln Arg Ala Gly Thr Ala Arg Ile Leu Lys Pro Ile Lys
165 170 175

Glu Pro Pro Val Gln Arg Arg Arg Gly Val Ser Leu Gly Pro Leu Glu
180 185 190

Ile His His Gly Val Gly Ser Lys Ala Pro Ala Ala Ala Arg Ala Lys
195 200 205

Pro Phe Thr Thr Lys Leu Asn Ala Ile Arg Glu Glu Thr Arg Pro Ser
210 215 220

Lys Gln Phe Ala Val Pro Ala Lys Pro Trp Pro Ser Ser Asn Thr Arg
225 230 235 240

Gln Thr Leu Asp Ser Arg Gln Gly Thr Ala Ala Ser Arg Ala Lys Ala
245 250 255

Arg Ser Pro Ser Pro Arg Pro Arg Arg Gln Ser Asn Gly Lys Ala Thr
260 265 270

Asp Thr Arg Gly Gly Asn Lys Val Val Asp Glu Leu Lys Pro Lys Gly
275 280 285

Ala Ser Ser Ser Gln Ser Gly Ser Ala Ala Ala Ala Ala Thr Ala Lys
290 295 300

Arg Met Ala Gly Ser Ser Lys Met Arg Val Ile Pro Ser Arg Tyr Ser
305 310 315 320

Leu Thr Pro Gly Ala Ser Leu Gly Ser Ser Gly Ala Gln Glu Arg Arg
325 330 335

Arg Lys Gln Ser Leu Pro Gly Ser Ser Gly Asp Ala Asn Gln Asn Glu
340 345 350

Glu Ile Arg Ala Lys Val Ile Glu Pro Ser Asn Asp Pro Leu Ser Pro
355 360 365

Gln Thr Ile Ser Lys Val Ala Glu Met Leu Pro Lys Ile Arg Thr Met
370 375 380

Pro Pro Pro Asp Glu Ser Pro Arg Asp Ser Gly Cys Ala Lys Arg Val
385 390 395 400

Ala Glu Leu Val Gly Lys Arg Ser Phe Phe Thr Ala Ala Ala Glu Asp
405 410 415

Gly Arg Ala Leu Asp Val Glu Ala Pro Glu Ala Val Ala Glu Ala
420 425 430

<210> 5
<211> 1860
<212> DNA
<213> Medicago trunculata

<220>
<221> misc_feature
<223> seedyl coding sequence

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aatcacatcg gagcgtgtat gagtagccgt ttcacatcca acggccagta agagcgtaac 180
tttatttctt ccctcttcaa tctccaacgg tcacataatc tcttccaaat acaaataatt 240
ccctctttca acctcactct tcatttcttc aacccaaacc caaaaaacta atcagattct 300
tcttaaatct tgaaaccttt ctcccaaaag cacttaaata aaaaagcact taaccatgaa 360

taacacaaac aacaacaaca ttcttcttca ttccacacag gttcaagtgt ggaacaacgc 420
agcattcgat ggtgaagatt tcgccatgaa ttcatcttct gattccatca aagagaatct 480
aaacccatcc gcattcaaca ttgttccttc ttcaaacaaa agaactattg atgatgaaat 540
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aaaagctgaa agaaaaatcg cttctgaaaa gcgtgttagt ggaattggta ctggaagaat 660
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tttcaaggag gagacaccga aacgaaacgg tgtcgtttcg gatacgccga aatctagggt 780
taattggaga agagggatga gtttaggtcc gatggagatt gccgggaaag tgatggcacc 840
gccggcgatg acgattactc cggcgacggt gaatcggagg aagtcttgtt tctggaaacc 900
gcaggaaagt tgtgaagtaa tgccgtcggg gattactccg gcgacggtga ataggaggaa 960
atcttgtttt ttgaaacctc aagaaagttg tgaagaaaat cgaagaaaaa cgatttgcaa 1020
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gaagaagaaa gatgaagaaa ttgctcaggt tcaaccgaag aagctgtttg aaggtgaaaa 1140
atcagtgaag aaatcgttga aacaaggtag aattgttgca agccggtata attccggtgg 1200
tggtggtggt gatgcgagga aaagatcgtt ttcggagaat aataagggtt tagggagtga 1260
aatcagggct aagaagagat gggagatacc aattgaagaa gtggatgtga gtggttttgt 1320
tatgttaccg aagatttcga caatgaggtt tgttgatgag agtcctagag attctggtgc 1380
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<210> 6
<211> 394
<212> PRT
<213> Medicago trunculata

<220>
<221> MISC_FEATURE
<223> seedy1 protein

<400> 6
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20 25 30

Ser Ser Ser Asp Ser Ile Lys Glu Asn Leu Asn Pro Ser Ala Phe Asn
35 40 45

Ile Val Pro Ser Ser Asn Lys Arg Thr Ile Asp Asp Glu Ile Ala Glu
50 55 60

Ile Glu Ser Glu Ile Lys Arg Leu Thr Ser Lys Leu Glu Leu Leu Arg
65 70 75 80

Val Glu Lys Ala Glu Arg Lys Ile Ala Ser Glu Lys Arg Val Ser Gly
85 90 95

Ile Gly Thr Gly Arg Ile Val Ala Ala Lys Phe Met Glu Pro Lys Lys
100 105 110

Asn Val Thr Pro Lys Arg Asn Gly Val Val Phe Lys Glu Glu Thr Pro
115 120 125

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Lys Arg Asn Gly Val Val Ser Asp Thr Pro Lys Ser Arg Val Asn Trp
    130                 135                 140

Arg Arg Gly Met Ser Leu Gly Pro Met Glu Ile Ala Gly Lys Val Met
145                 150                 155                 160

Ala Pro Pro Ala Met Thr Ile Thr Pro Ala Thr Val Asn Arg Arg Lys
                165                 170                 175

Ser Cys Phe Trp Lys Pro Gln Glu Ser Cys Glu Val Met Pro Ser Gly
            180                 185                 190

Ile Thr Pro Ala Thr Val Asn Arg Arg Lys Ser Cys Phe Leu Lys Pro
        195                 200                 205

Gln Glu Ser Cys Glu Glu Asn Arg Arg Lys Thr Ile Cys Lys Pro Asn
    210                 215                 220

Leu Asn Leu Asn Ser Asn Ser Val Asn Ser Ala Val Gly Ser Ile Lys
225                 230                 235                 240

Arg Val Lys Lys Lys Asp Glu Glu Ile Ala Gln Val Gln Pro Lys Lys
                245                 250                 255

Leu Phe Glu Gly Glu Lys Ser Val Lys Lys Ser Leu Lys Gln Gly Arg
            260                 265                 270

Ile Val Ala Ser Arg Tyr Asn Ser Gly Gly Gly Gly Gly Asp Ala Arg
        275                 280                 285

Lys Arg Ser Phe Ser Glu Asn Asn Lys Gly Leu Gly Ser Glu Ile Arg
    290                 295                 300

Ala Lys Lys Arg Trp Glu Ile Pro Ile Glu Glu Val Asp Val Ser Gly
305                 310                 315                 320

Phe Val Met Leu Pro Lys Ile Ser Thr Met Arg Phe Val Asp Glu Ser
                325                 330                 335

Pro Arg Asp Ser Gly Ala Val Lys Arg Val Ala Glu Leu Asn Gly Lys
            340                 345                 350

Arg Ser Tyr Phe Cys Asp Glu Asp Glu Glu Glu Arg Val Met Val Glu
        355                 360                 365

Glu Glu Gly Gly Ser Val Cys Gln Val Leu Asn Phe Ala Glu Asp Asp
    370                 375                 380

Asp Asp Asp Asp Asp Tyr Gly Glu Gln Gly
385                 390

<210>  7
<211>  674
<212>  DNA
<213>  Saccharum sp.

<220>
<221>  misc_feature
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<223> seedy1 coding sequence (partial 5' end)

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<221> misc_feature
<222> (362)..(362)
<223> n can be a, c, g or t

<220>
<221> misc_feature
<222> (372)..(372)
<223> n can be a, c, g or t

<220>
<221> misc_feature
<222> (674)..(674)
<223> n can be a, c, g or t

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gaagcaggaa tccctccgct cccagccgcc tcctccgctc acccatcgat cgatcgtccg 120
tccggtccag ggggctctcc ggcggcggtg gcgatggagg aggacccgct catcccgctg 180
gtgcacgtct ggaacaacgc cgccttcgac cacgcctcct cctccgcgtg gcacgcccac 240
tcccctgtgc ccgcgagcgc acgtcgcgag gcggaggggg acaaggagaa ccaccgcccc 300
gaccccgacc ccgacgtcga ggcggagatc ggccacatcg aggcggagat cctgcgcctg 360
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gggctcagcc tgggcccgct cgacgtcgcc gctgccggta accccaaccc gctcaccacc 540
gacaaccagc agcagcagcc gcgtgccgcg cagggtctga agccgatcaa gcaggccacg 600
gcggcggcgg gcaagggcgt aagacttggg ccccttcgac atggtcggcg cgaaccctag 660
ggtccctccg cccn 674

<210> 8
<211> 166
<212> PRT
<213> Saccharum sp.

<220>
<221> MISC_FEATURE
<223> seedy1 protein

<220>
<221> MISC_FEATURE
<223> seedy1 protein (partial N term)

<220>
<221> MISC_FEATURE
<222> (70)..(70)
<223> Xaa can be any amino acid

<400> 8
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Ala Phe Asp His Ala Ser Ser Ser Ala Trp His Ala His Ser Pro Val
20 25 30

Pro Ala Ser Ala Arg Arg Glu Ala Glu Gly Asp Lys Glu Asn His Arg
35 40 45

Pro Asp Pro Asp Pro Asp Val Glu Ala Glu Ile Gly His Ile Glu Ala
50 55 60

Glu Ile Leu Arg Leu Xaa Ser Arg Leu His His Leu Arg Thr Ser Lys
65 70 75 80

Gln Ser Glu Pro Ser Lys Arg Gly Glu Val Ala Pro Ala Pro Ala Ala
85 90 95

Lys Ala Lys Ala Ala Ala Ala Ala Arg Leu Arg Thr Arg Gly Leu Ser
100 105 110

Leu Gly Pro Leu Asp Val Ala Ala Ala Gly Asn Pro Asn Pro Leu Thr
115 120 125

Thr Asp Asn Gln Gln Gln Gln Pro Arg Ala Ala Gln Gly Leu Lys Pro
130 135 140

Ile Lys Gln Ala Thr Ala Ala Ala Gly Lys Gly Val Arg Leu Gly Pro
145 150 155 160

Leu Arg His Gly Arg Arg
165

<210> 9
<211> 876
<212> DNA
<213> Zea mays

<220>
<221> misc_feature
<223> seedy1 coding sequence (partial 3' end)

<220>
<221> misc_feature
<222> (869)..(869)
<223> n = a, c, g or t

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caagcagagc caaggcgagg agcgggagca taagccccag caggttcagg aggcagtcca 180
cttccaaggc tgccgagaca agagcgggaa atgccaagcc tacagaggcg acgaggggag 240
ggagcgaagc ggtcaatcac accagcaatg tagccacgac gaagaggccg gcggggagct 300
ccaaggtcag ggttgtcccg agccgctaca gcatcccacc tggctcctcc ctagcagctg 360
tgacacaagg caaccgatgc aagcagtctc tcccaggatc ggctactgag accagagtaa 420
atctcactga gccgccgaac gacgagttgt ctcctgaaga acttgccaag gttgcagagc 480
tgctcccaag gattaggacc atgccgcctt ctgatgagag cccgcgtgac tcgggatgtg 540
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cagaagaagc agaagcttga gaagtttgtc tttgatcaat tccgaagtgg cttgcatctg 720
ggcgtggcct ctttttgcag tgtgtgctac tacatagtct actgttacat tcatatcata 780
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aaagagagtg gaaggttcat ctgctgatnc cttgtt 876

<210> 10
<211> 224
<212> PRT
<213> Zea mays

<220>
<221> MISC_FEATURE
<223> seedy1 protein (partial C term)

<400> 10
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1 5 10 15

Ala Val Pro Ala Arg Pro Trp Pro Ser Ser Asn Ala Arg His Pro Leu
20 25 30

Asp Ala Arg Gln Gly Thr Ala Ala Ser Arg Ala Lys Ala Arg Ser Gly
35 40 45

Ser Ile Ser Pro Ser Arg Phe Arg Arg Gln Ser Thr Ser Lys Ala Ala
50 55 60

Glu Thr Arg Ala Gly Asn Ala Lys Pro Thr Glu Ala Thr Arg Gly Gly
65 70 75 80

Ser Glu Ala Val Asn His Thr Ser Asn Val Ala Thr Thr Lys Arg Pro
85 90 95

Ala Gly Ser Ser Lys Val Arg Val Val Pro Ser Arg Tyr Ser Ile Pro
100 105 110

Pro Gly Ser Ser Leu Ala Ala Val Thr Gln Gly Asn Arg Cys Lys Gln
115 120 125

Ser Leu Pro Gly Ser Ala Thr Glu Thr Arg Val Asn Leu Thr Glu Pro
130 135 140

Pro Asn Asp Glu Leu Ser Pro Glu Glu Leu Ala Lys Val Ala Glu Leu
145 150 155 160

Leu Pro Arg Ile Arg Thr Met Pro Pro Ser Asp Glu Ser Pro Arg Asp
165 170 175

Ser Gly Cys Ala Lys Arg Val Ala Asp Leu Val Gly Lys Arg Ser Phe
180 185 190

Phe Thr Ala Ala Gly Asp Asp Gly Asn Leu Val Thr Pro Tyr Gln Ala
195 200 205

Arg Val Val Glu Leu Glu Ser Pro Glu Ala Ala Ala Glu Glu Ala Glu
210 215 220

<210> 11
<211> 1257
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<223> seedy1 coding sequence

<400> 11
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aacgctgcct tcgacgatgg agattctcaa atcacttccg ccatcgaagc ttcttcttgg 120
tctcacctca acgaatcatt cgattccgat tgtagcaagg agaatcagtt tccgatttcg 180
gtttcctctt cgctccaatc ctcagtctcg atcaccgaag ctccgtcagc aaaatccaag 240
accgtgaaga ccaaatccgc cgcagatcgg agtaaaaagc gagatatcga tgcagagatc 300
gaagaagtag agaaggagat cggacgatta tcgacgaaat tggagtcgct ccgattagag 360
aaggcggagc aaaccgcaag aagcattgct atacgtggaa gaatcgttcc ggcgaagttc 420
atggaatcat ctcagaaaca agtgaaattc gacgattcgt gttttacagg atcgaaatca 480
agagccactc gtagaggcgt tagtcttgga ccagcggaga tattcaattc cgcgaagaaa 540
tctgaaactg tgactcctct tcaatcagct cagaatcgac gcaagtcttg tttctttaag 600
cttcctggaa tcgaagaagg tcaagtgacg acacgaggta aaggaagaac gagtttgagt 660
ctgagtccga gatctcgcaa agcgaaaatg acggcagctc agaagcaagc agctacgacg 720
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<211> 402
<212> PRT
<213> Arabidopsis thaliana

<220>
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<223> seedyl protein

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35 40 45

Ser Asp Cys Ser Lys Glu Asn Gln Phe Pro Ile Ser Val Ser Ser Ser
50 55 60

Leu Gln Ser Ser Val Ser Ile Thr Glu Ala Pro Ser Ala Lys Ser Lys
65 70 75 80

Thr Val Lys Thr Lys Ser Ala Ala Asp Arg Ser Lys Lys Arg Asp Ile
85 90 95

Asp Ala Glu Ile Glu Glu Val Glu Lys Glu Ile Gly Arg Leu Ser Thr
100 105 110

Lys Leu Glu Ser Leu Arg Leu Glu Lys Ala Glu Gln Thr Ala Arg Ser
115 120 125

Ile Ala Ile Arg Gly Arg Ile Val Pro Ala Lys Phe Met Glu Ser Ser
130 135 140

Gln Lys Gln Val Lys Phe Asp Asp Ser Cys Phe Thr Gly Ser Lys Ser

145 150 155 160

Arg Ala Thr Arg Arg Gly Val Ser Leu Gly Pro Ala Glu Ile Phe Asn
165 170 175

Ser Ala Lys Lys Ser Glu Thr Val Thr Pro Leu Gln Ser Ala Gln Asn
180 185 190

Arg Arg Lys Ser Cys Phe Phe Lys Leu Pro Gly Ile Glu Glu Gly Gln
195 200 205

Val Thr Thr Arg Gly Lys Gly Arg Thr Ser Leu Ser Leu Ser Pro Arg
210 215 220

Ser Arg Lys Ala Lys Met Thr Ala Ala Gln Lys Gln Ala Ala Thr Thr
225 230 235 240

Val Gly Ser Lys Arg Ala Val Lys Lys Glu Glu Gly Val Leu Leu Thr
245 250 255

Ile Gln Pro Lys Arg Leu Phe Lys Glu Asp Glu Lys Asn Val Ser Leu
260 265 270

Arg Lys Pro Leu Lys Pro Gly Arg Val Val Ala Ser Arg Tyr Ser Gln
275 280 285

Met Gly Lys Thr Gln Thr Gly Glu Lys Asp Val Arg Lys Arg Ser Leu
290 295 300

Pro Glu Asp Glu Glu Lys Glu Asn His Lys Arg Ser Glu Lys Arg Arg
305 310 315 320

Ala Ser Asp Glu Ser Asn Lys Ser Glu Gly Arg Val Lys Lys Arg Trp
325 330 335

Glu Ile Pro Ser Glu Val Asp Leu Tyr Ser Ser Gly Glu Asn Gly Asp
340 345 350

Glu Ser Pro Ile Val Lys Glu Leu Pro Lys Ile Arg Thr Leu Arg Arg
355 360 365

Val Gly Gly Ser Pro Arg Asp Ser Gly Ala Ala Lys Arg Val Ala Glu
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Leu Gln Ala Lys Asp Arg Asn Phe Thr Phe Cys Gln Leu Leu Lys Phe
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<210> 13
<211> 3074
<212> DNA
<213> Artificial sequence

<220>
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attgaaatta tataattcaa agagaataaa tccacatagc cgtaaagttc tacatgtggt 300
gcattaccaa aatatatata gcttacaaaa catgacaagc ttagtttgaa aaattgcaat 360
ccttatcaca ttgacacata aagtgagtga tgagtcataa tattattttc tttgctaccc 420
atcatgtata tatgatagcc acaaagttac tttgatgatg atatcaaaga acatttttag 480
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aatcctcatc atccttcacc acaattcaaa tattatagtt gaagcatagt agtaatttaa 660
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<211> 668
<212> DNA
<213> Oryza sativa

<220>
<221> misc_feature
<223> prolamin RP6 promter sequence

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gttattgtaa agttctacaa agctaattta aaagttattg cattaactta tttcatatta 180
caaacaagag tgtcaatgga acaatgaaaa ccatatgaca tactataatt ttgtttttat 240
tattgaaatt atataattca aagagaataa atccacatag ccgtaaagtt ctacatgtgg 300
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tccttatcac attgacacat aaagtgagtg atgagtcata atattatttt tcttgctacc 420
catcatgtat atatgatagc cacaaagtta ctttgatgat gatatcaaag aacattttta 480
ggtgcaccta acagaatatc caaataatat gactcactta gatcataata gagcatcaag 540
taaaactaac actctaaagc aaccgatggg aaagcatcta taaatagaca agcacaatga 600
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<210> 15
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<212> PRT
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<220>
<223> Motif 1 CORE SEQUENCE

<220>
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<222> (2)..(2)
<223> Xaa can be any amino acid

<220>
<221> MISC_FEATURE
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<223> Xaa can be any amino acid

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<210> 16
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<220>
<223> Motif 2 CORE SEQUENCE

<220>
<221> MISC_FEATURE
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Lys Glu Asn Xaa Xaa Pro
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<210> 17
<211> 15

<212> PRT
<213> Artificial sequence

<220>
<223> Motif 3 (coiled coil) CORE SEQUENCE

<220>
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<222> (2)..(2)
<223> Xaa can be a stretch of 1 to 6 amino acids

<220>
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<221> MISC_FEATURE
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<223> Xaa can be any amino acid

<220>
<221> MISC_FEATURE
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<400> 17
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<210> 18
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Motif 4 CORE SEQUENCE

<220>
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<222> (3)..(3)
<223> Xaa can be any amino acid

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa can be a stretch of 1 to 10 amino acids

<220>
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<223> Xaa can be any amino acid

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<221> MISC_FEATURE
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CD105PCT.ST25.txt

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